```
     Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
     Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
     Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
     Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
  5  Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
     Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
     Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
     Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
     Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 10  Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
     Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
     Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
     Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
     Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 15  Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
     Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
     Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
     Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
     Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 20  Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
     Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
     Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
     Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
     His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 25  Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
     Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
     Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
     Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
     His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 30  Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
     Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
     Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
     Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
     Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 35  Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
     Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
     Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
     Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
     Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 40  Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
     Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
     Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
     Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
     Leu Leu Met Glu Glu
 45
```

5.14 EXAMPLE 14 -- NUCLEIC ACID SEQUENCES OF THE GENES

ENCODING MODIFIED CRY1C* CRYSTAL PROTEINS

5.14.1 NUCLEIC ACID SEQUENCE OF *CRY1C-R148A* (SEQ ID NO:1)

5

10

15

20

25

30

35

40

45

50

```
ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAATTGTTTAAGTAATCCTGAAGAAGTACTTTTGGAT
GGAGAACGGATATCAACTGGTAATTCATCAATTGATATTTCTCTGTCACTTGTTCAGTTTCTGGTATCTAAC
TTTGTACCAGGGGGAGGATTTTTAGTTGGATTAATAGATTTGTATGGGGAATAGTTGGCCCTTCTCAATGG
GATGCATTTCTAGTACAAATTGAACAATTAATTAATGAAAGAATAGCTGAATTTGCTAGGAATGCTGCTATT
GCTAATTTAGAAGGATTAGGAAACAATTTCAATATATATGTGGAAGCATTTAAAGAATGGGAAGAAGATCCT
AATAATCCAGCAACCAGGACCAGAGTAATTGATCGCTTTCGTATACTTGATGGGCTACTTGAAAGGGACATT
CCTTCGTTTGCAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAGCGGCCAATCTGCATCTA
GCTATATTAAGAGATTCTGTAATTTTTGGAGAAAGATGGGGATTGACAACGATAAATGTCAATGAAAACTAT
AATAGACTAATTAGGCATATTGATGAATATGCTGATCACTGTGCAAATACGTATAATCGGGGATTAAATAAT
TTACCGAAATCTACGTATCAAGATTGGATAACATATAATCGATTACGGAGAGACTTAACATTGACTGTATTA
GATATCGCCGCTTTCTTTCCAAACTATGACAATAGGAGATATCCAATTCAGCCAGTTGGTCAACTAACAAGG
GAAGTTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCTGTAGCTCAATTACCTACTTTTAAC
GTTATGGAGAGCAGCGCAATTAGAAATCCTCATTTATTTGATATATTGAATAATCTTACAATCTTTACGGAT
TGGTTTAGTGTTGGACGCAATTTTTATTGGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGGTGGTAAC
ATAACATCTCCTATATATGGAAGAGAGGCGAACCAGGAGCCTCCAAGATCCTTTACTTTTAATGGACCGGTA
TTTAGGACTTTATCAAATCCTACTTTACGATTATTACAGCAACCTTGGCCAGCGCCACCATTTAATTTACGT
GGTGTTGAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTATCGAGGAAGAGGTACGGTTGATTCT
TTAACTGAATTACCGCCTGAGGATAATAGTGTGCCACCTCGCGAAGGATATAGTCATCGTTTATGTCATGCA
ACTTTTGTTCAAAGATCTGGAACACCTTTTTTAACAACTGGTGTAGTATTTTCTTGGACGCATCGTAGTGCA
ACTCTTACAAATACAATTGATCCAGAGAGAATTAATCAAATACCTTTAGTGAAAGGATTTAGAGTTTGGGGG
GGCACCTCTGTCATTACAGGACCAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACCTTTGGTGATTTT
GTATCTCTACAAGTCAATATTAATTCACCAATTACCCAAAGATACCGTTTAAGATTTCGTTACGCTTCCAGT
AGGGATGCACGAGTTATAGTATTAACAGGAGCGGCATCCACAGGAGTGGGAGGCCAAGTTAGTGTAAATATG
CCTCTTCAGAAAACTATGGAAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT
CCTTTTTCATTTAGAGCTAATCCAGATATAATTGGGATAAGTGAACAACCTCTATTTGGTGCAGGTTCTATT
AGTAGCGGTGAACTTTATATAGATAAAATTGAAATTATTCTAGCAGATGCAACATTTGAAGCAGAATCTGAT
TTAGAAAGAGCACAAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAATCAAATCGGGTTAAAAACCGATGTG
ACGGATTATCATATTGATCAAGTATCCAATTTAGTGGATTGTTTATCAGATGAATTTTGTCTGGATGAAAAG
CGAGAATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAAC
TTCAGAGGGATCAATAGACAACCAGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAGGAGGAGAT
GACGTATTCAAAGAGAATTACGTCACACTACCGGGTACCGTTGATGAGTGCTATCCAACGTATTTATATCAG
AAAATAGATGAGTCGAAATTAAAAGCTTATACCCGTTATGAATTAAGAGGGTATATCGAAGATAGTCAAGAC
TTAGAAATCTATTTGATCCGTTACAATGCAAAACACGAAATAGTAAATGTGCCAGGCACGGGTTCCTTATGG
CCGCTTTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT
CCTGATCTAGATTGTTCCTGCAGAGACGGGGAAAAATGTGCACATCATTCCCATCATTTCACCTTGGATATT
GATGTTGGATGTACAGACTTAAATGAGGACTTAGGTGTATGGGTGATATTCAAGATTAAGACGCAAGATGGC
CATGCAAGACTAGGGAATCTAGAGTTTCTCGAAGAGAAACCATTATTAGGGGAAGCACTAGCTCGTGTGAAA
AGAGCGGAGAAGAAGTGGAGAGACAAACGAGAGAAACTGCAGTTGGAAACAAATATTGTTTATAAAGAGGCA
AAAGAATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATAGATTACAAGTGGATACGAACATCGCAATG
ATTCATGCGGCAGATAAACGCGTTCATAGAATCCGGGAAGCGTATCTGCCAGAGTTGTCTGTGATTCCAGGT
GTCAATGCGGCCATTTTCGAAGAATTAGAGGGACGTATTTTTACAGCGTATTCCTTATATGATGCGAGAAAT
GTCATTAAAAATGGCGATTTCAATAATGGCTTATTATGCTGGAACGTGAAAGGTCATGTAGATGTAGAAGAG
CAAAACAACCACCGTTCGGTCCTTGTTATCCCAGAATGGGAGGCAGAAGTGTCACAAGAGGTTCGTGTCTGT
CCAGGTCGTGGCTATATCCTTCGTGTCACAGCATATAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCAT
GAGATCGAAGACAATACAGACGAACTGAAATTCAGCAACTGTGTAGAAGAGGAAGTATATCCAAACAACACA
GTAACGTGTAATAATTATACTGGGACTCAAGAAGAATATGAGGGTACGTACACTTCTCGTAATCAAGGATAT
GACGAAGCCTATGGTAATAACCCTTCCGTACCAGCTGATTACGCTTCAGTCTATGAAGAAAAATCGTATACA
GATGGACGAAGAGAGAATCCTTGTGAATCTAACAGAGGCTATGGGGATTACACACCACTACCGGCTGGTTAT
```

-143-

A 133020(2%N001° DOC)

GTAACAAAGGATTTAGAGTACTTCCCAGAGACCGATAAGGTATGGATTGAGATCGGAGAAACAGAAGGAACA
TTCATCGTGGATAGCGTGGAATTACTCCTTATGGAGGAA

5.14.2 NUCLEIC ACID SEQUENCE OF *CRY1C-R148D* (SEQ ID NO:3)

ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAATTGTTTAAGTAATCCTGAAGAAGTACTTTTGGAT
GGAGAACGGATATCAACTGGTAATTCATCAATTGATATTTCTCTGTCACTTGTTCAGTTTCTGGTATCTAAC
TTTGTACCAGGGGGAGGATTTTTAGTTGGATTAATAGATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGG
GATGCATTTCTAGTACAAATTGAACAATTAATTAATGAAAGAATAGCTGAATTTGCTAGGAATGCTGCTATT
GCTAATTTAGAAGGATTAGGAAACAATTTCAATATATATGTGGAAGCATTTAAAGAATGGGAAGAAGATCCT
AATAATCCAGCAACCAGGACCAGAGTAATTGATCGCTTTCGTATACTTGATGGGCTACTTGAAAGGGACATT
CCTTCGTTTGACATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAGCGGCCAATCTGCATCTA
GCTATATTAAGAGATTCTGTAATTTTTGGAGAAAGATGGGGATTGACAACGATAAATGTCAATGAAAACTAT
AATAGACTAATTAGGCATATTGATGAATATGCTGATCACTGTGCAAATACGTATAATCGGGGATTAAATAAT
TTACCGAAATCTACGTATCAAGATTGGATAACATATAATCGATTACGGAGAGACTTAACATTGACTGTATTA
-GATATCGCCGCTTTCTTTCCAAACTATGACAATAGGAGATATCCAATTCAGCCAGTTGGTCAACTAACAAGG
GAAGTTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCTGTAGCTCAATTACCTACTTTTAAC
GTTATGGAGAGCAGCGCAATTAGAAATCCTCATTTATTTGATATATTGAATAATCTTACAATCTTTACGGAT
TGGTTTAGTGTTGGACGCAATTTTTATTGGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGGTGGTAAC
ATAACATCTCCTATATATGGAAGAGAGGCGAACCAGGAGCCTCCAAGATCCTTTACTTTTAATGGACCGGTA
TTTAGGACTTTATCAAATCCTACTTTACGATTATTACAGCAACCTTGGCCAGCGCCACCATTTAATTTACGT
GGTGTTGAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTATCGAGGAAGAGGTACGGTTGATTCT
TTAACTGAATTACCGCCTGAGGATAATAGTGTGCCACCTCGCGAAGGATATAGTCATCGTTTATGTCATGCA
ACTTTTGTTCAAAGATCTGGAACACCCTTTTTTAACAACTGGTGTAGTATTTTCTTGGACGCATCGTAGTGCA
ACTCTTACAAATACAATTGATCCAGAGAGAATTAATCAAATACCTTTAGTGAAAGGATTTAGAGTTTGGGGG
GGCACCTCTGTCATTACAGGACCAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACCTTTGGTGATTTT
GTATCTACAAGTCAATATTAATTCACCAATTACCCAAAGATACCGTTTAAGATTTCGTTACGCTTCCAGT
AGGGATGCACGAGTTATAGTATTAACAGGAGCGGCATCCACAGGAGTGGGAGGCCAAGTTAGTGTAAATATG
CCTCTTCAGAAAACTATGGAAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT
CCTTTTTCATTTAGAGCTAATCCAGATATAATTGGGATAAGTGAACAACCTCTATTTGGTGCAGGTTCTATT
AGTAGCGGTGAACTTTATATAGATAAAATTGAAATTATTCTAGCAGATGCAACATTTGAAGCAGAATCTGAT
TTAGAAAGAGCACAAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAATCAAATCGGGTTAAAAACCGATGTG
ACGGATTATCATATTGATCAAGTATCCAATTTAGTGGATTGTTTATCAGATGAATTTTGTCTGGATGAAAAG
CGAGAATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAAC
TTCAGAGGGATCAATAGACAACCAGACCGTGGCTGGAGAGGAAGTACAGATATTACCATCCAAGGAGGAGAT
GACGTATTCAAAGAGAATTACGTCACACTACCGGGTACCGTTGATGAGTGCTATCCAACGTATTTATATCAG
AAAATAGATGAGTCGAAATTAAAAGCTTATACCCGTTATGAATTAAGAGGGTATATCGAAGATAGTCAAGAC
TTAGAAATCTATTTGATCCGTTACAATGCAAAACACGAAATAGTAAATGTGCCAGGCACGGGTTCCTTATGG
CCGCTTTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT
CCTGATCTAGATTGTTCCTGCAGAGACGGGGAAAAATGTGCACATCATTCCCATCATTTCACCTTGGATATT
GATGTTGGATGTACAGACTTAAATGAGGACTTAGGTGTATGGGTGATATTCAAGATTAAGACGCAAGATGGC
CATGCAAGACTAGGGAATCTAGAGTTTCTCGAAGAGAAACCATTATTAGGGGAAGCACTAGCTCGTGTGAAA
AGAGCGGAGAAGAAGTGGAGAGACAAACGAGAGAAACTGCAGTTGGAAACAAATATTGTTTATAAAGAGGCA
AAAGAATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATAGATTACAAGTGGATACGAACATCGCAATG
ATTCATGCGGCAGATAAACGCGTTCATAGAATCCGGGAAGCGTATCTGCCAGAGTTGTCTGTGATTCCAGGT
GTCAATGCGGCCATTTTCGAAGAATTAGAGGGACGTATTTTTACAGCGTATTCCTTATATGATGCGAGAAAT
GTCATTAAAAATGGCGATTTCAATAATGGCTTATTATGCTGGAACGTGAAAGGTCATGTAGATGTAGAAGAG
CAAAACAACCACCGTTCGGTCCTTGTTATCCCAGAATGGGAGGCAGAAGTGTCACAAGAGGTTCGTGTCTGT
CCAGGTCGTGGCTATATCCTTCGTGTCACAGCATATAAAGAGGGATATGGAGAGGGCTGCGTAACGATCCAT
GAGATCGAAGACAATACAGACGAACTGAAATTCAGCAACTGTGTAGAAGAGGAAGTATATCCAAACAACACA
GTAACGTGTAATAATTATACTGGGACTCAAGAAGAATATGAGGGTACGTACACTTCTCGTAATCAAGGATAT
GACGAAGCCTATGGTAATAACCCTTCCGTACCAGCTGATTACGCTTCAGTCTATGAAGAAAAATCGTATACA
GATGGACGAAGAGAGAATCCTTGTGAATCTAACAGAGGCTATGGGGATTACACACCACTACCGGCTGGTTAT